Journal of MOLECULAR BIOLOGY

Editors in Chief
J. C. KENDREW S. BRENNER

Editors

P. Chambon
G. A. Gilbert
M. Gottesman
I. Herskowitz
R. Huber
H. E. Huxley
A. Klug
B. Mach
K. Matsubara

Associate Editors

C. R. Cantor
V. Luzzati
J. H. Miller
M. F. Moody

Volume 186

5 November to 20 December 1985

ACADEMIC PRESS

(Harcourt Brace Jovanovich, Publishers)

London Orlando San Diego New York
Toronto Montreal Sydney Tokyo

Copyright © 1985, by Academic Press Inc. (London) Ltd.

ALL RIGHTS RESERVED

No part of this volume may be reproduced in any form, by photostat, microfilm, or any other means, without written permission from the publishers.

Printed in Great Britain

Contents of Volume 186

Number 1, 5 November 1985

Diekmann, S. and Wang, J. C., On the Sequence Determinants and Flexibility of the Kinetoplast DNA Fragment with Abnormal Gel Electrophoretic Mobilities . . . 1

Buckland, R. A. and Elder, J. K., On the Mechanism of Amplification of Satellite II DNA Sequences of the Domestic Goat *Capra hircus* 13

Buckland, R. A., Sequence and Evolution of Related Bovine and Caprine Satellite DNAs. Identification of a Short DNA Sequence Potentially Involved in Satellite DNA Amplification 25

Reis, R. J. S., Srivastava. A., Beranek, D. T. and Goldstein, S., Human Alphoid Family of Tandemly Repeated DNA. Sequence of Cloned Tetrameric Fragments and Analysis of Familial Divergence 31

Shelly, C. S., Sharpe, C. R., Baralle, F. E. and Shoulders, C. C., Comparison of the Human Apolipoprotein Genes. Apo AII Presents a Unique Functional Intron–Exon Junction 43

Hecht, M. H. and Sauer, R. T., Phage Lambda Repressor Revertants. Amino Acid Substitutions that Restore Activity to Mutant Proteins 53

Fuller-Pace, F. V., Cowan, G. M. and Murray, N. E., *Eco*A and *Eco*E: Alternatives to the *Eco*K Family of Type I Restriction and Modification Systems of *Escherichia coli* . 65

Suri, B. and Bickle, T. A., *Eco*A: The First Member of a New Family of Type I Restriction Modification Systems. Gene Organization and Enzymatic Activities . . 77

Dooley, T. P., Tamm, J. and Polisky, B., Isolation and Characterization of Mutants Affecting Functional Domains of ColE1 RNAI 87

Toman, Z., Dambly-Chaudière, C., Tenebaum, L. and Radman, M., A System for Detection of Genetic and Epigenetic Alterations in *Escherichia coli* Induced by DNA-damaging Agents 97

Ohta, N., Chen, L.-S., Swanson, E. and Newton, A., Transcriptional Regulation of a Periodically Controlled Flagellar Gene Operon in *Caulobacter crescentus* . . . 107

Galas, D. J., Eggert, M. and Waterman, M. S., Rigorous Pattern-recognition Methods for DNA Sequences. Analysis of Promoter Sequences from *Escherichia coli* . . . 117

Hay, R. T., Origin of Adenovirus DNA Replication. Role of the Nuclear Factor I Binding Site *in Vivo* 129

Berger, E. M., Vitek, M. P. and Morganelli, C. M., Transcript Length Heterogeneity at the Small Heat Shock Protein Genes of *Drosophila* 137

Vincent, A., Colot, H. V. and Rosbash, M., Sequence and Structure of the *Serendipity* Locus of *Drosophila melanogaster*. A Densely Transcribed Region Including a Blastoderm-specific Gene 149

Greulich, K. O., Ausio, J. and Eisenberg, H., Nucleosome Core Particle Structure and Structural Changes in Solution 167

Appendix: Analytical Estimation of the Smearing by a Trapezoid Beam Profile . . 172

Foote, J. and Schachman, H. K., Homotropic Effects in Aspartate Transcarbamoylase. What Happens when the Enzyme Binds a Single Molecule of the Bisubstrate Analog *N*-Phosphonacetyl-L-Aspartate? 175

Hartzell, H. C., Effects of Phosphorylated and Unphosphorylated C-protein on Cardiac Actomyosin ATPase 185

Letters to the Editor

Rümbeli, R., Schirmer, T., Bode, W., Sidler, W. and Zuber, H., Crystallization of Phycoerythrocyanin from the Cyanobacterium *Mastigocladus laminosus* and Preliminary Characterization of Two Crystal Forms 197

Chang, C.-H., Schiffer, M., Tiede, D., Smith, U. and Norris, J., Characterization of Bacterial Photosynthetic Reaction Center Crystals from *Rhodopseudomonas sphaeroides* R-26 by X-ray Diffraction 201

Bjorkman, P. J., Strominger, J. L. and Wiley, D. C., Crystallization and X-ray Diffraction Studies on the Histocompatibility Antigens HLA-A2 and HLA-A28 from Human Cell Membranes 205

Bignetti, E., Tirindelli, R., Rossi, G. L., Bolognesi, M., Coda, A. and Gatti, G., Crystallization of an Odorant-binding Protein from Cow Nasal Mucosa . . . 211

Morris, D. C., Searcy, D. G. and Edwards, B. F. P., Crystallization of a Fe,Zn Superoxide Dismutase from the Archaebacterium *Thermoplasma acidophilium* . 213

Sygusch, J. and Beaudry, D., Preliminary Crystallographic Investigation of Rabbit Liver Aldolase 215

Number 2, 20 November 1985

Andronico, F., De Lucchini, S., Graziani, F., Nardi, I., Batistoni, R. and Barsacchi-Pilone, G., Molecular Organization of Ribosomal RNA Genes Clustered at Variable Chromosomal Sites in *Triturus vulgaris meridionalis* (Amphibia, Urodela) . . . 219

Burger, G. and Werner, S., The Mitochondrial URF1 Gene in *Neurospora crassa* has an Intron that Contains a Novel Type of URF 231

Hardin, S. H., Carpenter, C. D., Hardin, P. E., Bruskin, A. M. and Klein, W. H., Structure of the Spec1 Gene Encoding a Major Calcium-binding Protein in the Embryonic Ectoderm of the Sea Urchin, *Strongylocentrotus purpuratus* 243

Fukuda, M., Wakasugi, S., Tsuzuki, T., Nomiyama, H., Shimada, K. and Miyata, T., Mitochondrial DNA-like Sequences in the Human Nuclear Genome. Characterization and Implications in the Evolution of Mitochondrial DNA 257

Horowitz, B. and Deonier, R. C., Formation of Δ*tra* F′ Plasmids: Specific Recombination at *oriT* 267

Banfalvi, G. and Sarkar, N., Origin and Degradation of the RNA Primers at the 5′ Termini of Nascent DNA Chains in *Bacillus subtilis* 275

Joyce, C. M., Fujii, D. M., Laks, H. S., Hughes, C. M. and Grindley, N. D. F., Genetic Mapping and DNA Sequence Analysis of Mutations in the *polA* Gene of *Escherichia coli* 283

Mossing, M. C. and Record, M. T. Jr, Thermodynamic Origins of Specificity in the *lac* Repressor–Operator Interaction. Adaptability in the Recognition of Mutant Operator Sites 295

Sedivy, J. M. and Fraenkel, D. G., Fructose Bisphosphatase of *Saccharomyces cerevisiae*. Cloning, Disruption and Regulation of the *FBP1* Structural Gene 307

Romans, P. and Firtel, R. A., Organization of the Actin Multigene Family of *Dictyostelium discoideum* and Analysis of Variability in the Protein Coding Regions . 321

Romans, P., Firtel, R. A. and Saxe, C. L. III., Gene-specific Expression of the Actin Multigene Family of *Dictyostelium discoideum* 337

Grossman, A. D., Taylor, W. E., Burton, Z. F., Burgess, R. R. and Gross, C. A., Stringent Response in *Escherichia coli* Induces Expression of Heat Shock Proteins . 357

Marion, C., Martinage, A., Tirard, A., Roux, B., Daune, M. and Mazen, A., Histone Phosphorylation in Native Chromatin Induces Local Structural Changes as Probed by Electric Birefringence 367

Bähler, M., Eppenberger, H. M. and Wallimann, T., Novel Thick Filament Protein of Chicken Pectoralis Muscle: the 86 kd Protein. I. Purification and Characterization . 381

Bähler, M., Eppenberger, H. M. and Wallimann, T., Novel Thick Filament Protein of Chicken Pectoralis Muscle: the 86 kd Protein. II. Distribution and Localization . . 393

Kilchherr, E., Hofmann, H., Steigemann, W. and Engel, J., Structural Model of the Collagen-like Region of C1q Comprising the Kink Region and the Fibre-like Packing of the Six Triple Helices 403

Sowadski, J. M., Handschumacher, M. D., Krishna Murthy, H. M., Foster, B. A. and Wyckoff, H. W., Refined Structure of Alkaline Phosphatase from *Escherichia coli* at 2·8 Å Resolution 417

Clore, G. M., Gronenborn, A. M., Brünger, A. T. and Karplus, M., Solution Conformation of a Heptadecapeptide Comprising the DNA Binding Helix F of the Cyclic AMP Receptor Protein of *Escherichia coli*. Combined use of ^{1}H Nuclear Magnetic Resonance and Restrained Molecular Dynamics 435

Letters to the Editor

Dennis, P. P., Multiple Promoters for the Transcription of the Ribosomal RNA Gene Cluster in *Halobacterium cutirubrum* 457

Gupta, G., Sarma, M. H. and Sarma, R. H., Secondary Structure of the Hybrid Poly(rA)·Poly(dT) in Solution. Studies Involving NOE at 500 MHz and Stereochemical Modelling Within the Constraints of NOE Data 463

Perutz, M. F., Gronenborn, A. M., Clore, G. M., Shih, D. T.-b. and Craescu, C. T., Comparison of Histidine Proton Magnetic Resonances of Human Carbonmonoxyhaemoglobin in Different Buffers 471

Schiffer, M., Chang, C.-H. and Stevens, F. J., Formation of an Infinite β-Sheet Arrangement Dominates the Crystallization Behaviour of λ-Type Antibody Light Chains 475

Guddat, L. W., Cowan, S. W., Machin, K. J., Isaacs, N. W. and Cotton, R. G. H., Crystallization and Preliminary Crystallographic Data of the Fab Fragment of an Anti-phenylalanine Hydroxylase Monoclonal Antibody 479

Tsukihara, T., Fukuyama, K., Wakabayashi, S., Wada, K., Matsubara, H., Kerscher, L. and Oesterhelt, D., Preliminary X-ray Diffraction Studies on a Ferredoxin from the Thermophilic Archaebacterium, *Thermoplasma acidophilum* . 481

Number 3, 5 December 1985

Meneveri, R., Agresti, A., Della Valle, G., Talarico, D., Siccardi, A. G. and Ginelli, E., Identification of a Human Clustered G+C-rich DNA Family of repeats (*Sau*3A Family) 483

Schubiger, J.-L., Germond, J.-E., ten Heggeler, B. and Wahli, W., The Vi Element. A Transposon-like Repeated DNA Sequence Interspersed in the Vitellogenin Locus of *Xenopus laevis* 491

Reha-Krantz, L. J. and Lambert, J. K. J., Structure–Function Studies of the Bacteriophage T4 DNA Polymerase. Isolation of a Novel Suppressor Mutant . . 505

Symington, L. S., Morrison, P. and Kolodner, R., Intramolecular Recombination of Linear DNA Catalyzed by the *Escherichia coli RecE* Recombination System . . 515

Guidi-Rontani, C. and Spassky, A., RNA Polymerase Mutant Able to Express *in Vivo* and *in Vitro* the Lactose Operon in the Absence of the cAMP-CRP Complex . . 527

Daldal, F. and Applebaum, J., Cloning and Expression of *Clostridium pasteurianum* Galactokinase Gene in *Escherichia coli* K-12 and Nucleotide Sequence Analysis of a Region Affecting the Amount of the Enzyme 533

Peschke, U., Beuck, V., Bujard, H., Gentz, R. and Le Grice, S., Efficient Utilization of *Escherichia coli* Transcriptional Signals in *Bacillus subtilis* 547

Durand-Tardif, M., Broglie, R., Slightom, J. and Tepfer, D., Structure and Expression of Ri T-DNA from *Agrobacterium rhizogenes* in *Nicotiana tabacum*. Organ and Phenotypic Specificity 557

Cusack, S., Ruigrok, R. W. H., Krygsman, P. C. J. and Mellema, J. E., Structure and Composition of Influenza Virus. A Small-angle Neutron Scattering Study . . . 565

Appendix 1: The Spherical Shell Model-fitting Technique 577

Appendix 2: Simulation of Scattering from Surface Spikes on Spherical Viruses . . 579

Hamodrakas, S. J., Etmektzoglou, T. and Kafatos, F. C., Amino Acid Periodicities and Their Structural Implications for the Evolutionarily Conservative Central Domain of some Silkmoth Chorion Proteins 583

Chou, K.-C., Némethy, G., Rumsey, S., Tuttle, R. W. and Scheraga, H. A., Interactions Between an α-Helix and a β-Sheet. Energetics of α/β Packing in Proteins 591

Appendix A 607

Appendix B 608

Appendix C 608

Braun, W. and Gō, N., Calculation of Protein Conformations by Proton– Proton Distance Constraints. A New Efficient Algorithm 611

Finzel, B. C., Weber, P. C., Hardman, K. D. and Salemme, F. R., Structure of Ferricytochrome *c′* from *Rhodospirillum molischianum* at 1·67 Å Resolution. . . . 627

Warwicker, J., Ollis, D., Richards, F. M. and Steitz, T. A., Electrostatic Field of the Large Fragment of *Escherichia coli* DNA Polymerase I 645

Chothia, C., Novotný, J., Bruccoleri, R. and Karplus, M., Domain Association in Immunoglobulin Molecules. The Packing of Variable Domains 651

Letters to the Editor

Keller, B., Kellenberger, E., Bickle, T. A. and Tsugita, A., Determination of the Cleavage Site of the Phage T4 Prohead Protease in Gene Product 68. Influence of Protein Secondary Structure on Cleavage Specificity 665

Sirdeshmukh, R. and Schlessinger, D., Why is Processing of 23 S Ribosomal RNA in *Escherichia coli* not Obligate for its Function? 669

Abdel-Meguid, S. S., Smith, W. W. and Bild, G. S., Crystallization of 5-Enolpyruvylshikimate 3-Phosphate Synthase from *Escherichia coli* 673

Tanaka, Y., Takahashi, S., Mitsui, Y., Itoh, S., Iitaka, Y., Kasai, H. and Okuyama, T., X-ray Crystallographic and Chromatographic Characterization of the Crystals of Ca^{2+}–Calmodulin Complexed with Bee Venom Melittin 675

Number 4, 20 December 1985

Chia, W., Savakis, C., Karp, R., Pelham, H. and Ashburner, M., Mutation of the *Adh* Gene of *Drosophila melanogaster* Containing an Internal Tandem Duplication . . . 679

Chia, W., Karp, R., McGill, S. and Ashburner, M., Molecular Analysis of the *Adh* Region of the Genome of *Drosophila melanogaster*. 689

Cunin, R., Jacobs, A., Charlier, D., Crabeel, M., Hervé, G., Glansdorff, N. and Piérard, A., Structure–Function Relationship in Allosteric Aspartate Carbamoyltransferase from *Escherichia coli*. I. Primary Structure of a *pyrI* Gene Encoding a Modified Regulatory Subunit 707

Ladjimi, M. M., Ghelis, C., Feller, A., Cunin, R., Glansdorff, N., Piérard, A. and Hervé, G., Structure–Function Relationship in Allosteric Aspartate Carbamoyltransferase from *Escherichia coli*. II. Involvement of the C-Terminal Region of the Regulatory Chain in Homotropic and Heterotropic Interactions 715

Cone, K. C. and Steege, D. A., Messenger RNA Conformation and Ribosome Selection of Translational Reinitiation Sites in the *lac* Repressor mRNA 725

Cone, K. C. and Steege, D. A., Functional Analysis of *lac* Repressor Restart Sites in Translational Initiation and Reinitiation 733

Spadafora, C. and Riccardi, P., Different Conformations of Ribosomal DNA in Active and Inactive Chromatin in *Xenopus laevis* 743

Feiss, M., Sippy, J. and Miller, G., Processive Action of Terminase During Sequential Packaging of Bacteriophage λ Chromosomes. 759

Drew, H. R. and Travers, A. A., DNA Bending and its Relation to Nucleosome Positioning 773

Wei, L.-N. and Joys, T. M., Covalent Structure of Three Phase-1 Flagellar Filament Proteins of *Salmonella* 791

Kneale, G., Brown, T., Kennard, O. and Rabinovich, D., G·T Base-pairs in a DNA Helix: The Crystal Structure of d(G-G-G-G-T-C-C-C) 805

Zauhar, R. J. and Morgan, R. S., A New Method for Computing the Macromolecular Electric Potential 815

Letter to the Editor

Lorch, Y. and Kornberg, R. D., A Region Flanking the *GAL7* Gene and a Binding Site for *GAL4* Protein as Upstream Activating Sequences in Yeast 821

Index to Volume 186

ABDEL-MEGUID, S. S. SMITH, W. W. & BILD, G. S., Crystallization of 5-enolpyruvylshikimate 3-phosphate synthase from *Escherichia coli*, 673

Actin multigene family of *Dictyostelium discoideum*, gene-specific expression, 337

Actin multigene family organization in *Dictyostelium discoideum*, and analysis of variability in the protein coding regions, 321

Actomyosin ATPase, cardiac, and effects of phosphorylated and unphosphorylated C-protein, 185

Adenovirus DNA, origin of replication; role of the nuclear factor I binding site *in vivo*, 129

Adh gene of *Drosophila melanogaster*, a mutation containing an internal tandem duplication, 679

Adh region of the genome of *Drosophila melanogaster*, molecular analysis, 689

AGRESTI, A. (see also MENEVERI, R.), 483

Agrobacterium rhizogenes Ri T-DNA, structure and expression in *Nicotiana tabacum*; organ and phenotypic specificity, 557

Aldolase, rabbit liver, preliminary crystallographic investigation, 215

Alkaline phosphatase from *Escherichia coli*, refined structure at 2·8 Å resolution, 417

Alphoid family, human, of tandemly repeated DNA. Sequence of cloned tetrameric fragments and analysis of familial divergence, 31

Amino acid periodicities and their structural implications for the evolutionarily conservative central domain of some silkmoth chorion proteins, 583

Amino acid substitutions that restore activity to mutant proteins; phage lambda repressor revertants, 53

Amplification mechanism of satellite II DNA sequences of the domestic goat *Capra hircus*, 13

ANDRONICO, F., DE LUCCHINI, S., GRAZIANI, F., NARDI, I., BATISTONI, R. & BARSACCHI-PILONE, G., Molecular organization of ribosomal RNA genes clustered at variable chromosomal sites in *Triturus vulgaris meridionalis* (Amphibia, Urodela), 219

Antibody light chains, λ-type, formation of an infinite β-sheet arrangement dominates the crystallization behavior, 475

Antigens HLA-A2 and HLA-A28 from human cell membranes, crystallization and X-ray diffraction studies, 205

Anti-phenylalanine hydroxylase monoclonal antibody, crystallization and preliminary crystallographic data of the Fab fragment, 479

ASHBURNER, M. (see also CHIA, W.), 679

Aspartate carbamoyltransferase from *Escherichia coli*, structure–function relationship; involvement of the C-terminal region of the regulatory chain in homotropic and heterotropic interactions, 715

Aspartate carbamoyltransferase from *Escherichia coli*, structure–function relationship; primary structure of a *pyrI* gene encoding a modified regulatory subunit, 707

Aspartate transcarbamoylase, homotropic effects. What happens when the enzyme binds a single molecule of the bisubstrate analog *N*-phosphonacetyl-L-aspartate?, 175

Apolipoprotein genes, human, a comparison; apo AII presents a unique functional intron–exon junction, 43

APPLEBAUM, J. (see also DALDAL, F.), 533

AUSIO, J. (see also GREULICH, K. O.), 167

Bacillus subtilis, efficient utilization of *Escherichia coli* transcriptional signals, 547

Bacillus subtilis, origin and degradation of the RNA primers at the 5′ termini of nascent DNA chains, 275

Bacterial photosynthetic reaction center crystals from *Rhodopseudomonas sphaeroides* R-26, characterization by X-ray diffraction, 201

BÄHLER, M., EPPENBERGER, H. M. & WALLIMANN, T., Novel thick filament protein of chicken pectoralis muscle: the 86 kd protein. I. Purification and characterization, 381

BÄHLER, M., EPPENBERGER, H. M. & WALLIMANN, T., Novel thick filament protein of chicken pectoralis muscle: the 86 kd protein. II. Distribution and localization, 393

BANFALVI, G. & SARKAR, N., Origin and degradation of the RNA primers at the 5′ termini of nascent DNA chains in *Bacillus subtilis*, 275

BARALLE, F. E. (see also SHELLY, C. S.), 43

BARSACCHI-PILONE, G. (see also ANDRONICO, F.), 219

BATISTONI, R. (see also ANDRONICO, F.), 219

BEAUDRY, D. (see also SYGUSCH, J.), 215

Bee venom melittin complexed with Ca^{2+}-calmodulin, X-ray crystallographic and chromatographic characterization of crystals, 675

BERANEK, D. T. (see also REIS, R. J. S.), 31

BERGER, E. M., VITEK, M. P. & MORGANELLI, C. M., Transcript length heterogeneity at the small heat shock locus protein genes of *Drosophila*, 137

BEUCK, V. (see also PESCHKE, U.), 547

BICKLE, T. A. (see also KELLER, B.), 665

BICKLE, T. A. (see also SURI, B.), 77

BIGNETTI, E., TIRINDELLI, R., ROSSI, G. L., BOLOGNESI, M., CODA, A. & GATTI, G., Crystallization of an odorant-binding protein from cow nasal mucosa, 211

BILD, G. S. (see also ABDEL-MEGUID, S. S.), 573

BJORKMAN, P. J., STROMINGER, J. L. & WILEY, D. C., Crystallization and X-ray diffraction studies on the histocompatibility antigens HLA-A2 and HLA-A28 from human cell membranes, 205

Blastoderm-specific gene; sequence and structure of the *Serendipity* locus of *Drosophila melanogaster*, 149

BODE, W. (see also RÜMBELI, R.), 197

BOLOGNESI, M. (see also BIGNETTI, E.), 211

Bovine and caprine related satellite DNAs, sequence and evolution; identification of a short DNA sequence potentially involved in satellite DNA amplification, 25

BRAUN, W. & GŌ, N., Calculation of protein conformations by proton–proton distance constraints. A new efficient algorithm, 611

BROGLIE, R. (see also DURAND-TARDIF, M.), 557

BROWN, T. (see also KNEALE, G.), 805

BRUCCOLERI, R. (see also CHOTHIA, C.), 651

BRÜNGER, A. T. (see also CLORE, G. M.), 435

BRUSKIN, A. M. (see also HARDIN, S. H.), 243

BUCKLAND, R. A., Sequence and evolution of related bovine and caprine satellite DNAs. Identification of a short DNA sequence potentially involved in satellite DNA amplification, 25

BUCKLAND, R. A. & ELDER, J. K., On the mechanism of amplification of satellite II DNA sequences of the domestic goat *Capra hircus*, 13

Buffers, different, and comparison of histidine proton n.m.r. of human carbonmonoxyhaemoglobin, 471

BUJARD, H. (see also PESCHKE, U.), 547

BURGER, G. & WERNER, S., The mitochondrial URF1 gene in *Neurospora crassa* has an intron that contains a novel type of URF, 231

BURGESS, R. R. (see also GROSSMAN, A. D.), 357

BURTON, Z. F. (see also GROSSMAN, A. D.), 357

Calcium-binding protein in the embryonic ectoderm of the sea urchin, *Strongylocentrotus purpuratus*; structure of the encoding Spec1 gene, 243

Ca^{2+}-calmodulin complexed with bee venom melittin, X-ray crystallographic and chromatographic characterization of crystals, 675

Calmodulin: X-ray crystallographic and chromatographic characterization of the crystals of Ca^{2+}-calmodulin complexed with bee venom melittin, 675

Capra hircus, on the mechanism of amplification of satellite II DNA sequences, 13

Caprine and bovine related satellite DNAs, sequence and evolution; identification of a short DNA sequence potentially involved in satellite DNA amplification, 25
Carbonmonoxyhaemoglobin, human, comparison of histidine proton n.m.r. in different buffers, 471
Cardiac actomyosin ATPase, effects of phosphorylated and unphosphorylated C-protein, 185
Carpenter, C. D. (see also Hardin, S. H.), 243
Caulobacter crescentus, transcriptional regulation of a periodically controlled flagellar gene operon, 107
Cell membranes, human, crystallization and X-ray diffraction studies on the histocompatibility antigens HLA-A2 and HLA-A28, 205
Chang, C.-H., Schiffer, M., Tiede, D., Smith, U. & Norris, J., Characterization of bacterial photosynthetic reaction center crystals from *Rhodopseudomonas sphaeroides* R-26 by X-ray diffraction, 201
Chang, C.-H. (see also Schiffer, M.), 475
Charlier, D. (see also Cunin, R.), 707
Chen, L.-S. (see also Ohta, N.), 107
Chia, W., Karp, R., McGill, S. & Ashburner, M., Molecular analysis of the *Adh* region of the genome of *Drosophila melanogaster*, 689
Chia, W., Savakis, C., Karp, R., Pelham, H. & Ashburner, M., Mutation of the *Adh* gene of *Drosophila melanogaster* containing an internal tandem duplication, 679
Chicken pectoralis muscle, the novel thick filament 86 kd protein; distribution and localization, 393
Chicken pectoralis muscle, the novel thick filament 86 kd protein; purification and characterization, 381
Chorion proteins, silkmoth; amino acid periodicities and their structural implications for the evolutionarily conservative central domain, 583
Chothia, C., Novotný, J., Bruccoleri, R. & Karplus, M., Domain association in immunoglobulin molecules. The packing of variable domains, 651
Chou, K.-C., Némethy, G., Rumsey, S., Tuttle, R. W. & Scheraga, H. A., Interactions between an α-helix and a β-sheet. Energetics of α/β packing in proteins, 591
Chromatin, active and inactive, in *Xenopus laevis*, has different conformations of ribosomal DNA, 743
Chromatin, native, histone phosphorylation induces local structural changes as probed by electric birefringence, 367
Chromatographic characterization of the crystals of Ca^{2+}-calmodulin complexed with bee venom melittin, 675
Chromosomes, phage λ, and processive action of terminase during sequential packaging, 759
Cleavage site of the phage T4 prohead protease in gene product 68. Influence of protein secondary structure on cleavage specificity, 665
Cloned tetrameric fragment sequences, and analysis of familial divergence; human alphoid family of tandemly repeated DNA, 31
Cloning, disruption and regulation of the *FBP1* structural gene from *Saccharomyces cerevisiae*, 307
Cloning and expression of *Clostridium pasteurianum* galactokinase gene in *Escherichia coli* K-12 and nucleotide sequence analysis of a region affecting the amount of the enzyme, 533
Clore, G. M., Gronenborn, A. M., Brünger, A. T. & Karplus, M., Solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of *Escherichia coli*. Combined use of ^1H nuclear magnetic resonance and restrained molecular dynamics, 435
Clore, G. M. (see also Perutz, M. F.), 471
Clostridium pasteurianum galactokinase gene, cloning and expression in *Escherichia coli* K-12, and nucleotide sequence analysis of a region affecting the amount of the enzyme, 533
Coda, A. (see also Bignetti, E.), 211
ColE1 RNAI, isolation and characterization of mutants affecting functional domains, 87
Collagen-like region of C1q comprising the kink region and the fibre-like packing of the six triple helices; a structural model, 403
Colot, H. V. (see also Vincent, A.), 149
Cone, K. C. & Steege, D. A., Functional analysis of *lac* repressor restart sites in translational initiation and reinitiation, 733
Cone, K. C. & Steege, D. A., Messenger RNA conformation and ribosome selection of translational reinitiation sites in the *lac* repressor mRNA, 725
Conformation, mRNA, and ribosome selection of translational reinitiation sites in the *lac* repressor mRNA, 725
Conformation, solution, of a heptadecapeptide comprising the DNA binding helix F of the cyclic AMP receptor protein of *Escherichia coli*. Combined use of ^1H n.m.r. and restrained molecular dynamics, 435
Conformations, different, of ribosomal DNA in active and inactive chromatin in *Xenopus laevis*, 743
Conformations of proteins, calculation by proton–proton distance constraints; a new efficient algorithm, 611
Cotton, R. G. H. (see also Guddat, L. W.), 479
Cow nasal mucosa, crystallization of an odorant-binding protein, 211
Cowan, G. M. (see also Fuller-Pace, F. V.), 65
Cowan, S. W. (see also Guddat, L. W.), 479
C1q, structural model of the collagen-like region, comprising the kink region and the fibre-like packing of the six triple helices, 403
Crabeel, M. (see also Cunin, R.), 707
Craescu, C. T. (see also Perutz, M. F.), 471
Crystal structure of d(G-G-G-G-T-C-C-C), 805
Crystals of Ca^{2+}-calmodulin complexed with bee venom melittin, X-ray crystallographic and chromatographic characterization, 675
Crystallization behavior of λ-type antibody light chains is dominated by formation of infinite β-sheet arrangement, 475
Crystallization of 5-enolpyruvylshikimate 3-phosphate synthase from *Escherichia coli*, 673
Crystallization of a Fe,Zn superoxide dismutase from the Archaebacterium *Thermoplasma acidophilium*, 213
Crystallization of an odorant-binding protein from cow nasal mucosa, 211
Crystallization of phycoerythrocyanin from the cyanobacterium *Mastigocladus laminosus* and preliminary characterization of two crystal forms, 197
Crystallization and preliminary crystallographic data of the Fab fragment of an anti-phenylalanine hydroxylase monoclonal antibody, 479
Crystallization and X-ray diffraction studies on the histocompatibility antigens HLA-A2 and HLA-A28 from human cell membranes, 205
Crystallographic data, preliminary, of the Fab fragment of an anti-phenylalanine hydroxylase monoclonal antibody, 479
Crystallographic investigation, preliminary, of rabbit liver aldolase, 215
Cunin, R., Jacobs, A., Charlier, D., Crabeel, M., Hervé, G., Glansdorff, N. & Piérard, A., Structure–function relationship in allosteric aspartate carbamoyltransferase from *Escherichia coli*. I. Primary structure of a *pyrI* gene encoding a modified regulatory subunit, 707
Cunin, R. (see also Ladjimi, M. M.), 715
Cusack, S., Ruigrok, R. W. H., Krygsman, P. C. J. & Mellema, J. E., Structure and composition of influenza virus. A small-angle neutron scattering study, 565
Cyanobacterium *Mastigocladus laminosus* phycoerythrocyanin, crystallization and preliminary characterization of two crystal forms, 197
Cyclic AMP receptor protein of *Escherichia coli*, solution conformation of a heptadecapeptide comprising the DNA binding helix F; combined use of n.m.r. and restrained molecular dynamics, 435
cAMP-CRP complex absence, and the ability of RNA polymerase mutant to express *in vivo* and *in vitro* the lactose operon, 527

Daldal, F. & Applebaum, J., Cloning and expression of *Clostridium pasteurianum* galactokinase gene in *Escherichia coli* K-12 and nucleotide sequence analysis of a region affecting the amount of the enzyme, 533
Dambly-Chaudière, C. (see also Toman, Z.), 97
Daune, M. (see also Marion, C.), 367
Δ*tra* F′ plasmid formation: specific recombination at *oriT*, 267
Della Valle, G. (see also Meneveri, R.), 483
De Lucchini, S. (see also Andronico, F.), 219

Dennis, P. P., Multiple promoters for the transcription of the ribosomal RNA gene cluster in *Halobacterium cutirubrum*, 157
Deonier, R. C. (see also Horowitz, B.), 267
DNA, adenovirus, origin of replication; role of the nuclear factor I binding site *in vivo*, 129
DNA bending and its relation to nucleosome positioning, 773
DNA binding helix F of cAMP receptor protein of *Escherichia coli*, solution conformation; combined use of n.m.r. and restrained molecular dynamics, 435
DNA chains, nascent, in *Bacillus subtilis*, origin and degradation of the RNA primers at the 5′ termini, 275
DNA damage: a system for detection of genetic and epigenetic alterations in *Escherichia coli*, 97
DNA family, G+C-rich, clustered, human, of repeats (*Sau*3A family), 483
DNA fragment, kinetoplast, with abnormal gel electrophoretic mobilities, sequence determinants and flexibility, 1
DNA helix G·T base-pairs: the crystal structure of d(G-G-G-G-T-C-C-C), 805
DNA, linear, intramolecular recombination catalyzed by the *Escherichia coli recE* recombination system, 515
DNA polymerase I, *Escherichia coli*, electrostatic field of the large fragment, 645
DNA polymerase, T4, structure–function studies; isolation of a novel suppressor mutant, 505
DNA, ribosomal, different conformations in active and inactive chromatin in *Xenopus laevis*, 743
DNA, satellite II, sequences of the domestic goat, *Capra hircus*; the mechanism of amplification, 13
DNA sequence analysis of mutations in the *polA* gene of *Escherichia coli*, 283
DNA sequence, repeated, transposon-like, interspersed in the vitellogenin locus of *Xenopus laevis*; the Vi element, 491
DNA sequences, rigorous pattern-recognition methods; analysis of promoter sequences from *Escherichia coli*, 117
DNA, tandemly repeated, human alphoid family; sequence of cloned tetrameric fragments and analysis of familial divergence, 31
DNAs, satellite, bovine and caprine, sequence and evolution; identification of a short DNA sequence potentially involved in satellite DNA amplification, 25
DNA-like sequences in the human nuclear genome; characterization and implications in the evolution of mitochondrial DNA, 257
T-DNA, Ri, from *Agrobacterium rhizogenes*, structure and expression in *Nicotiana tabacum*; organ and phenotypic specificity, 557
d(G-G-G-G-T-C-C-C) crystal structure, 805
Dictyostelium discoideum, gene-specific expression of the actin multigene family, 337
Dictyostelium discoideum, organization of the actin multigene family, and analysis of variability in the protein coding regions, 321
Diekmann, S. & Wang, J. C., On the sequence determinants and flexibility of the kinetoplast DNA fragment with abnormal gel electrophoretic mobilities, 1
Domain association in immunoglobulin molecules. The packing of variable domains, 651
Dooley, T. P., Tamm, J. & Polisky, B., Isolation and characterization of mutants affecting functional domains of ColE1 RNAI, 87
Drew, H. R. & Travers, A. A., DNA bending and its relation to nucleosome positioning, 773
Drosophila melanogaster, molecular analysis of the *Adh* region of the genome, 689
Drosophila melanogaster, mutation of the *Adh* gene containing an internal tandem duplication, 679
Drosophila melanogaster, sequence and structure of the *Serendipity* locus. A densely transcribed region including a blastoderm-specific gene, 149
Drosophila, transcript length heterogeneity at the small heat shock protein genes, 137
Duplication, tandem, internal, of the *Drosophila Adh* gene, 679
Durand-Tardif, M., Broglie, R., Slightom, J. & Tepfer, D., Structure and expression of Ri T-DNA from *Agrobacterium rhizogenes* in *Nicotiana tabacum*. Organ and phenotypic specificity, 557
*Eco*A: the first member of a new family of type I restriction modification systems. Gene organization and enzymatic activities, 77
*Eco*A and *Eco*E: alternatives to the *Eco*K family of type I restriction and modification systems of *Escherichia coli*, 65
Edwards, B. F. P. (see also Morris, D. C.), 213
Efficient utilization of *Escherichia coli* transcriptional signals in *Bacillus subtilis*, 547
Eggert, M. (see also Galas, D. J.), 117
Eisenberg, H. (see also Greulich, K. O.), 167
Elder, J. K. (see also Buckland, R. A.), 13
Electric birefringence probe of local structural changes induced by histone phosphorylation in native chromatin, 367
Electric potential, macromolecular, a new method for computation, 815
Electrostatic field of the large fragment of *Escherichia coli* DNA polymerase I, 645
Embryonic ectoderm of the sea urchin, *Strongylocentrotus purpuratus*, and structure of the Spec1 gene encoding a major calcium-binding protein, 243
Energetics of α/β packing in proteins. Interactions between an α-helix and a β-sheet, 591
Engel, J. (see also Kilchherr, E.), 403
5-Enolpyruvylshikimate 3-phosphate synthase from *Escherichia coli*; crystallization, 673
Eppenberger, H. M. (see also Bähler, M.), 381, 393
Escherichia coli alkaline phosphatase, refined structure at 2·8 Å resolution, 417
Escherichia coli, analysis of promoter sequences by rigorous pattern-recognition methods, 117
Escherichia coli, crystallization of 5-enolpyruvylshikimate 3-phosphate synthase, 673
Escherichia coli DNA polymerase I, electrostatic field of the large fragment, 645
Escherichia coli, *Eco*A, the first member of a new family of restriction modification systems; gene organization and enzymatic activities, 77
Escherichia coli, *Eco*A and *Eco*E: alternatives to the *Eco*K family of type I restriction and modification systems, 65
Escherichia coli, genetic mapping and DNA sequence analysis of mutations in the *polA* gene, 283
Escherichia coli recE recombination system, and catalysis of intramolecular recombination of linear DNA, 515
Escherichia coli, stringent response induces expression of heat shock proteins, 357
Escherichia coli, structure–function relationship in allosteric aspartate carbamoyltransferase; involvement of the C-terminal region of the regulatory chain in homotropic and heterotropic interactions, 715
Escherichia coli, structure–function relationship in allosteric aspartate carbamoyltransferase; primary structure of a *pyrI* gene encoding a modified regulatory subunit, 707
Escherichia coli, solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cAMP receptor protein; combined use of n.m.r. and restrained molecular dynamics, 435
Escherichia coli, a system for detection of genetic and epigenetic alterations induced by DNA-damaging agents, 97
Escherichia coli transcriptional signals efficiently used in *Bacillus subtilis*, 547
Escherichia coli, why is processing of 23 S ribosomal RNA not obligate for its function?, 669
Escherichia coli K-12, cloning and expression of *Clostridium pasteurianum* galactokinase gene, and nucleotide sequence analysis of a region affecting the amount of the enzyme, 533
Etmektzoglou, T. (see also Hamodrakas, S. J.), 583
Evolution of mitochondrial DNA; implications of mitochondrial DNA-like sequences in the human nuclear genome, 257
Evolution of related bovine and caprine satellite DNAs. Identification of a short DNA sequence potentially involved in satellite DNA amplification, 25
Evolutionarily conservative central domain of some silkmoth chorion proteins, amino acid periodicities and their structural implications, 583
Expression of heat shock proteins is induced by stringent response in *Escherichia coli*, 357

Mitochondrial DNA-like sequences in the human nuclear genome. Characterization and implications in the evolution of mitochondrial DNA, 257
Mitochondrial URF1 gene in *Neurospora crassa* has an intron that contains a novel type of URF, 231
Mitsui, Y. (see also Tanaka, Y.), 675
Miyata, T. (see also Fukuda, M.), 257
Molecular analysis of the *Adh* region of the genome of *Drosophila melanogaster*, 689
Monoclonal antibody, anti-phenylalanine hydroxylase, crystallization and preliminary crystallographic data of the Fab fragment, 479
Morgan, R. S. (see also Zauhar, R. J.), 815
Morganelli, C. M. (see also Berger, E. M.), 137
Morris, D. C., Searcy, D. G. & Edwards, B. F. P., Crystallization of a Fe,Zn superoxide dismutase from the Archaebacterium *Thermoplasma acidophilium*, 213
Morrison, P. (see also Symington, L. S.), 515
Mossing, M. C. & Record, M. T. Jr, Thermodynamic origins of specificity in the *lac* repressor–operator interaction. Adaptability in the recognition of mutant operator sites, 295
Murray, N. E. (see also Fuller-Pace, F. V.), 65
Muscle, pectoralis, chicken, the 86 kd novel thick filament protein; distribution and localization, 393
Muscle, pectoralis, chicken, the 86 kd novel thick filament protein; purification and characterization, 381
Mutant operator sites, adaptability in recognition; thermodynamic origins of specificity in the *lac* repressor–operator interaction, 295
Mutant proteins, and amino acid substitutions that restore their activity; phage lambda repressor revertants, 53
Mutant, RNA polymerase, able to express *in vivo* and *in vitro* the lactose operon in the absence of the cAMP-CRP complex, 527
Mutant, suppressor, novel, isolation; structure–function studies of T4 DNA polymerase, 505
Mutants affecting functional domains of ColE1 RNAI, isolation and characterization, 87
Mutation of the *Adh* gene of *Drosophila melanogaster* containing an internal tandem duplication, 679
Mutations in the *polA* gene of *Escherichia coli*, genetic mapping and DNA sequence analysis, 283

Nardi, I. (see also Andronico, F.), 219
Nasal mucosa of cow, crystallization of an odorant-binding protein, 211
Némethy, G. (see also Chou, K.-C.), 591
Neurospora crassa, the mitochondrial URF1 gene has an intron that contains a novel type of URF, 231
Neutron scattering study of structure and composition of influenza virus, 565
Newton, A. (see also Ohta, N.), 107
Nicotiana tabacum, structure and expression of Ri T-DNA from *Agrobacterium rhizogenes*; organ and phenotypic specificity, 557
NOE studies at 500 MHz of the secondary structure of the hybrid poly(rA)·poly(dT), 463
Nomiyama, H. (see also Fukuda, M.), 257
Norris, J. (see also Chang, C.-H.), 201
Novotný, J. (see also Chothia, C.), 651
N-phosphonacetyl-L-aspartate, what happens when the enzyme binds a single molecule?; homotropic effects in aspartate transcarbamoylase, 175
Nuclear factor I binding site, role *in vivo* in adenovirus DNA replication, 129
Nuclear magnetic resonance, ^1H, combined with restrained molecular dynamics in determination of solution conformation of a heptadecapeptide comprising the DNA binding helix F of the cAMP receptor protein of *Escherichia coli*, 435
Nuclear magnetic resonances, proton, histidine, of human carbonmonoxyhaemoglobin, comparison in different buffers, 471
Nucleosome core particle structure and structural changes in solution, 167
Nucleosome positioning and its relation to DNA bending, 773
Odorant-binding protein from cow nasal mucosa; crystallization, 211
Oesterhelt, D. (see also Tsukihara, T.), 481
Ohta, N., Chen, L.-S., Swanson, E. & Newton, A., Transcriptional regulation of a periodically controlled flagellar gene operon in *Caulobacter crescentus*, 107
Okuyama, T. (see also Tanaka, Y.), 675
Organization of the actin multigene family of *Dictyostelium discoideum* and analysis of variability in the protein coding regions, 321
Organization, molecular, of ribosomal RNA genes clustered at variable chromosomal sites in *Triturus vulgaris meridionalis* (Amphibia, Urodela), 219
oriT specific recombination, and formation of Δ*tra* F′ plasmids, 267

Packaging, sequential, of bacteriophage λ chromosomes, and processive action of terminase, 759
Packing, α/β, in proteins; interactions between an α-helix and a β-sheet, 591
Packing of variable domains; domain association in immunoglobulin molecules, 651
Pattern-recognition methods, rigorous, for DNA sequences. Analysis of promoter sequences from *Escherichia coli*, 117
Pelham, H. (see also Chia, W.), 679
Perutz, M. F., Gronenborn, A. M., Clore, G. M., Shih, D. T.-B & Craescu, C. T., Comparison of histidine proton magnetic resonances of human carbonmonoxyhaemoglobin in different buffers, 471
Peschke, U., Beuck, V., Bujard, H., Gentz, R. & Le Grice, S., Efficient utilization of *Escherichia coli* transcriptional signals in *Bacillus subtilis*, 547
Phage λ chromosomes, processive action of terminase during sequential packaging, 759
Phage lambda repressor revertants. Amino acid substitutions that restore activity to mutant proteins, 53
Phage T4 DNA polymerase, structure–function studies; isolation of a novel suppressor mutant, 505
Phage T4 prohead protease, determination of the cleavage site in gene product 68. Influence of protein secondary structure on cleavage specificity, 665
Phosphorylated and unphosphorylated C-protein, effects on cardiac actomyosin ATPase, 185
Phosphorylation, histone, in native chromatin induces local structural changes as probed by electric birefringence, 367
Photosynthetic bacterial reaction center crystals from *Rhodopseudomonas sphaeroides* R-26, characterization by X-ray diffraction, 201
Phycoerythrocyanin crystallization from the cyanobacterium *Mastigocladus laminosus*, and preliminary characterization of two crystal forms, 197
Piérard, A. (see also Cunin, R.), 707
Piérard, A. (see also Ladjimi, M. M.), 715
Plasmid, Δ*tra* F′, formation: specific recombination at *oriT*, 267
polA gene of *Escherichia coli*, genetic mapping and DNA sequence analysis of mutations, 283
Polisky, B. (see also Dooley, T. P.), 87
Poly(rA)·poly(dT) hybrid, secondary structure in solution. NOE studies at 500 MHz and stereochemical modelling, 463
Processive action of terminase during sequential packaging of bacteriophage λ chromosomes, 759
Prohead protease, T4, determination of the cleavage site in gene product 68; influence of protein secondary structure on cleavage specificity, 665
Promoter sequences from *Escherichia coli*, analysis by rigorous pattern-recognition methods, 117
Promoters, multiple, for the transcription of the ribosomal RNA gene cluster in *Halobacterium cutirubrum*, 457
Protein, calcium-binding, in the embryonic ectoderm of the sea urchin, *Strongylocentrotus purpuratus*; structure of the encoding SpecI gene, 243
Protein coding region variability for the actin multigene family of *Dictyostelium discoideum*, 321
Protein conformations, calculation by proton–proton distance constraints; a new efficient algorithm, 611
Protein, odorant-binding, from cow nasal mucosa; crystallization, 211

Protein, thick filament, 86 kd, of chicken pectoralis muscle; distribution and localization, 393
Protein, thick filament, 86 kd, of chicken pectoralis muscle; purification and characterization, 381
C-protein, phosphorylated and unphosphorylated, effects on cardiac actomyosin ATPase, 185
Proteins, chorion, silkmoth; amino acid periodicities and their structural implications for the evolutionarily conservative central domain, 583
Proteins, energetics of α/β packing; interactions between an α-helix and a β-sheet, 591
Proteins, flagellar filament, of *Salmonella*; covalent structure, 791
Proton–proton distance constraint calculation of protein conformations; a new efficient algorithm, 611
pyrI gene encoding a modified regulatory subunit, primary structure; structure–function relationship in allosteric aspartate carbamoyltransferase from *Escherichia coli*, 707

Rabbit liver aldolase, preliminary crystallographic investigation, 215
Rabinovich, D. (see also Kneale, G.), 805
Radman, M. (see also Toman, Z.), 97
Reaction center crystals, bacterial photosynthetic, from *Rhodopseudomonas sphaeroides* R-26, characterization by X-ray diffraction, 201
Recombination, intramolecular, of linear DNA catalyzed by the *Escherichia coli recE* recombination system, 515
Recombination, specific, at *oriT*, and formation of Δtra F′ plasmids, 267
Record, M. T. Jr (see also Mossing, M. C.), 295
Regulation of the *FBP1* structural gene from *Saccharomyces cerevisiae*, 307
Regulation, transcriptional, of a periodically controlled flagellar gene operon in *Caulobacter crescentus*, 107
Regulatory chain, involvement of the C-terminal region in homotropic and heterotropic interactions; aspartate carbamoyltransferase from *Escherichia coli*, 715
Regulatory subunit, modified, and the primary structure of an encoding *pyrI* gene; aspartate carbamoyltransferase from *Escherichia coli*, 707
Reha-Krantz, L. J. & Lambert, J. K. J., Structure–function studies of the bacteriophage T4 DNA polymerase. Isolation of a novel suppressor mutant, 505
Reis, R. J. S., Srivastava, A., Beranek, D. T. & Goldstein, S., Human alphoid family of tandemly repeated DNA. Sequence of cloned tetrameric fragments and analysis of familial divergence, 31
Replication of adenovirus DNA, role of the nuclear factor I binding site *in vivo*, 129
Repressor revertants, phage lambda; amino acid substitutions that restore activity to mutant proteins, 53
Restriction modification systems: *Eco*A, the first member of a new family; gene organization and enzymatic activities, 77
Restriction and modification systems of *Escherichia coli*. *Eco*A and *Eco*E: alternatives to the *Eco*K family, 65
Revertants, repressor, phage lambda; amino acid substitutions that restore activity to mutant proteins, 53
Rhodopseudomonas sphaeroides R-26, X-ray diffraction characterization of bacterial photosynthetic reaction center crystals, 201
Rhodospirillum molischianum ferricytochrome *c′*, structure at 1·67 Å resolution, 627
Ri T-DNA from *Agrobacterium rhizogenes*, structure and expression in *Nicotiana tabacum*; organ and phenotypic specificity, 557
Ribosomal DNA, different conformations in active and inactive chromatin in *Xenopus laevis*, 743
Ribosomal RNA gene cluster in *Halobacterium cutirubrum*, multiple promoters for transcription, 457
Ribosomal RNA genes clustered at variable chromosomal sites in *Triturus vulgaris meridionalis* (Amphibia, Urodela); molecular organization study, 219
Ribosomal 23 S RNA, why is processing in *Escherichia coli* not obligate for its function?, 669
Riccardi, P. (see also Spadafora, C.), 743
Richards, F. M. (see also Warwicker, J.), 645
RNA polymerase mutant able to express *in vivo* and *in vitro* the lactose operon in the absence of the cAMP-CRP complex, 527
RNA primers, origin and degradation, at the 5′ termini of nascent DNA chains in *Bacillus subtilis*, 275
RNA, ribosomal, gene cluster in *Halobacterium cutirubrum*, multiple promoters for transcription, 457
RNA ribosomal genes clustered at variable chromosomal sites in *Triturus vulgaris meridionalis* (Amphibia, Urodela); molecular organization study, 219
RNA, 23 S ribosomal, why is processing in *Escherichia coli* not obligate for its function?, 669
RNAI, ColE1, isolation and characterization of mutants affecting functional domains, 87
Romans, P. & Firtel, R. A., Organization of the actin multigene family of *Dictyostelium discoideum* and analysis of variability in the protein coding regions, 321
Romans, P., Firtel, R. A. & Saxe, C. L. III., Gene-specific expression of the actin multigene family of *Dictyostelium discoideum*, 337
Rosbash, M. (see also Vincent, A.), 149
Rossi, G. L. (see also Bignetti, E.), 211
Roux, B. (see also Marion, C.), 367
Ruigrok, R. W. H. (see also Cusack, S.), 565
Rümbeli, R., Schirmer, T., Bode, W., Sidler, W. & Zuber, H., Crystallization of phycoerythrocyanin from the cyanobacterium *Mastigocladus laminosus* and preliminary characterization of two crystal forms, 197
Rumsey, S. (see also Chou, K.-C.), 591

Saccharomyces cerevisiae fructose bisphosphatase. Cloning, disruption and regulation of the *FBP1* structural gene, 307
Salemme, F. R. (see also Finzel, B. C.), 627
Salmonella, covalent structure of three phase-1 flagellar filament proteins, 791
Sarkar, N. (see also Banfalvi, G.), 275
Sarma, M. H. (see also Gupta, G.), 463
Sarma, R. H. (see also Gupta, G.), 463
Satellite DNAs, bovine and caprine, sequence and evolution; identification of a short DNA sequence potentially involved in satellite DNA amplification, 25
Satellite II DNA sequences of the domestic goat *Capra hircus*, on the mechanism of amplification, 13
*Sau*3A family: identification of a human clustered G+C-rich DNA family of repeats, 483
Sauer, R. T. (see also Hecht, M. H.), 53
Savakis, C. (see also Chia, W.), 679
Saxe, C. L. III. (see also Romans, P.), 337
Scattering from surface spikes on spherical viruses, 579
Schachman, H. K. (see also Foote, J.), 175
Scheraga, H. A. (see also Chou, K.-C.), 591
Schiffer, M., Chang, C.-H. & Stevens, F. J., Formation of an infinite β-sheet arrangement dominates the crystallization behaviour of λ-type antibody light chains, 475
Schiffer, M. (see also Chang, C.-H.), 201
Schirmer, T. (see also Rümbeli, R.), 197
Schlessinger, D. (see also Sirdeshmukh, R.), 669
Schubiger, J.-L., Germond, J.-E., ten Heggeler, B. & Wahli, W., The Vi element. A transposon-like repeated DNA sequence interspersed in the vitellogenin locus of *Xenopus laevis*, 491
Searcy, D. G. (see also Morris, D. C.), 213
Sedivy, J. M. & Fraenkel, D. G., Fructose bisphosphatase of *Saccharomyces cerevisiae*. Cloning, disruption and regulation of the *FBP1* structural gene, 307
Sequence analysis of mutations in the *polA* gene of *Escherichia coli*, 283
Sequence of cloned tetrameric fragments and analysis of familial divergence; human alphoid family of tandemly repeated DNA, 31
Sequence determinants and flexibility of the kinetoplast DNA fragment with abnormal gel electrophoretic mobilities, 1
Sequence, DNA, repeated, transposon-like, interspersed in the vitellogenin locus of *Xenopus laevis*; the Vi element, 491
Sequence and evolution of related bovine and caprine satellite

DNAs. Identification of a short DNA sequence potentially involved in satellite DNA amplification, 25
Sequence, nucleotide, analysis of a region affecting the amount of enzyme; cloning and expression of *Clostridium pasteurianum* galactokinase gene in *Escherichia coli* K-12, 533
Sequence and structure of the *Serendipity* locus of *Drosophila melanogaster*. A densely transcribed region including a blastoderm-specific gene, 149
Sequences activating, upstream, in yeast; a region flanking the *GAL7* gene and a binding site for *GAL4* protein, 821
Sequences, DNA, and rigorous pattern-recognition methods; analysis of promoter sequences from *Escherichia coli*, 117
Sequences, mitochondrial DNA-like, in the human nuclear genome; characterization and implications in the evolution of mitochondrial DNA, 257
Sequences, satellite II DNA, of the domestic goat *Capra hircus*; the mechanism of amplification, 13
Serendipity locus of *Drosophila melanogaster*, sequence and structure; a densely transcribed region including a blastoderm-specific gene, 149
Sharpe, C. R. (see also Shelly, C. S.), 43
β-Sheet, interactions with α-helix. Energetics of α/β packing in proteins, 591
β-Sheet formation dominates the crystallization behavior of λ-type antibody light chains, 475
Shelly, C. S., Sharpe, C. R., Baralle, F. E. & Shoulders, C. C., Comparison of the human apolipoprotein genes. Apo AII presents a unique functional intron–exon junction, 43
Shih, D. T.-b. (see also Perutz, M. F.), 471
Shimada, K. (see also Fukuda, M.), 257
Shoulders, C. C. (see also Shelly, C. S.), 43
Siccardi, A. G. (see also Meneveri, R.), 483
Sidler, W. (see also Rümbeli, R.), 197
Silkmoth chorion proteins, amino acid periodicities and their structural implications for the evolutionarily conservative central domain, 583
Sippy, J. (see also Feiss, M.), 759
Sirdeshmukh, R. & Schlessinger, D., Why is processing of 23 S ribosomal RNA in *Escherichia coli* not obligate for its function?, 669
Slightom, J. (see also Durand-Tardif, M.), 557
Smearing by a trapezoid beam profile, analytical estimation, 172
Smith, U. (see also Chang, C.-H.), 201
Smith, W. W. (see also Abdel-Meguid, S. S.), 673
Sowadski, J. M., Handschumacher, M. D., Krishna Murthy, H. M., Foster, B. A. & Wyckoff, H. W., Refined structure of alkaline phosphatase from *Escherichia coli* at 2·8 Å resolution, 417
Spadafora, C. & Riccardi, P., Different conformations of ribosomal DNA in active and inactive chromatin in *Xenopus laevis*, 743
Spassky, A. (see also Guidi-Rontani, C.), 527
Spec1 gene encoding a major calcium-binding protein in the embryonic ectoderm of the sea urchin, *Strongylocentrotus purpuratus*; study of gene structure, 243
Specificity in the *lac* repressor–operator interaction, thermodynamic origins; adaptability in the recognition of mutant operator sites, 295
Spherical shell model-fitting technique, 577
Spherical viruses, simulation of scattering from surface spikes, 579
Srivastava, A. (see also Reis, R. J. S.), 31
Steege, D. A. (see also Cone, K. C.), 725, 733
Steigemann, W. (see also Kilchherr, E.), 403
Steitz, T. A. (see also Warwicker, J.), 645
Stevens, F. J. (see also Schiffer, M.), 475
Stringent response in *Escherichia coli* induces expression of heat shock proteins, 357
Strominger, J. L. (see also Bjorkman, P. J.), 205
Strongylocentrotus purpuratus, structure of the Spec1 gene encoding a major calcium-binding protein in the embryonic ectoderm, 243
Structural changes, local, induced by histone phosphorylation in native chromatin, as probed by electric birefringence, 367
Structural implications of amino acid periodicities for the evolutionarily conservative central domain of some silkmoth chorion proteins, 583
Structural model of the collagen-like region of C1q comprising the kink region and the fibre-like packing of the six triple helices, 403
Structure and composition of influenza virus. A small-angle neutron scattering study, 565
Structure, covalent, of three phase-1 flagellar filament proteins of *Salmonella*, 791
Structure, crystal, of d(G-G-G-G-T-C-C-C), 805
Structure and expression of Ri T-DNA from *Agrobacterium rhizogenes* in *Nicotiana tabacum*. Organ and phenotypic specificity, 557
Structure of ferricytochrome *c'* from *Rhodospirillum molischianum* at 1·67 Å resolution, 627
Structure of nucleosome core particles, and structural changes in solution, 167
Structure, refined, of alkaline phosphatase from *Escherichia coli* at 2·8 Å resolution, 417
Structure, secondary, of the hybrid poly(rA)·poly(dT) in solution. Studies involving NOE at 500 MHz and stereochemical modelling within the constraints of NOE data, 463
Structure, secondary, protein, influence on cleavage specificity; determination of the cleavage site of the phage T4 prohead protease in gene product 68, 665
Structure of the *Serendipity* locus of *Drosophila melanogaster*. A densely transcribed region including a blastoderm-specific gene, 149
Structure of the Spec1 gene encoding a major calcium-binding protein in the embryonic ectoderm of the sea urchin, *Strongylocentrotus purpuratus*, 243
Structure–function relationship in allosteric aspartate carbamoyltransferase from *Escherichia coli*. Involvement of the C-terminal region of the regulatory chain in homotropic and heterotropic interactions, 715
Structure–function relationship in allosteric aspartate carbamoyltransferase from *Escherichia coli*. Primary structure of a *pyrI* gene encoding a modified regulatory subunit, 707
Structure–function studies of the phage T4 DNA polymerase. Isolation of a novel suppressor mutant, 505
Superoxide dismutase, Fe,Zn, from the Archaebacterium *Thermoplasma acidophilium*; crystallization, 213
Suppressor mutant, novel, isolation; structure–function studies of T4 DNA polymerase, 505
Surface spike scattering for spherical viruses, 579
Suri, B. & Bickle, T. A., *Eco*A: the first member of a new family of type I restriction modification systems. Gene organization and enzymatic activities, 77
Swanson, E. (see also Ohta, N.), 107
Sygusch, J. & Beaudry, D., Preliminary crystallographic investigation of rabbit liver aldolase, 215
Symington, L. S., Morrison, P. & Kolodner, R., Intramolecular recombination of linear DNA catalyzed by the *Escherichia coli RecE* recombination system, 515

T4 (see also Phage), 505, 665
Takahashi, S. (see also Tanaka, Y.), 675
Talarico, D. (see also Meneveri, R.), 483
Tamm, J. (see also Dooley, T. P.), 87
Tanaka, Y., Takahashi, S., Mitsui, Y., Itoh, S., Iitaka, Y., Kasai, H. & Okuyama, T., X-ray crystallographic and chromatographic characterization of the crystals of Ca^{2+}-calmodulin complexed with bee venom melittin, 675
Tandemly repeated DNA, human alphoid family; sequence of cloned tetrameric fragments and analysis of familial divergence, 31
Taylor, W. E. (see also Grossman, A. D.), 357
Tenebaum, L. (see also Toman, Z.), 97
ten Heggeler, B. (see also Schubiger, J.-L.), 491
Tepfer, D. (see also Durand-Tardif, M.), 557
Terminase processive action during sequential packaging of bacteriophage λ chromosomes, 759
Thermodynamic origins of specificity in the *lac* repressor–operator interaction. Adaptability in the recognition of mutant operator sites, 295
Thermophilic Archaebacterium, *Thermoplasma acidophilum*, preliminary X-ray diffraction studies on a ferredoxin, 481

Thermoplasma acidophilium Archaebacterium, crystallization of a Fe,Zn superoxide dismutase, 213
Thermoplasma acidophilum, preliminary X-ray diffraction studies on a ferredoxin, 481
Thick filament protein of chicken pectoralis muscle: the 86 kd protein; distribution and localization, 393
Thick filament protein of chicken pectoralis muscle: the 86 kd protein; purification and characterization, 381
Tiede, D. (see also Chang, C.-H.), 201
Tirard, A. (see also Marion, C.), 367
Tirindelli, R. (see also Bignetti, E.), 211
Toman, Z., Dambly-Chaudière, C., Tenebaum, L. & Radman, M., A system for detection of genetic and epigenetic alterations in *Escherichia coli* induced by DNA-damaging agents, 97
Transcript length heterogeneity at the small heat shock protein genes of *Drosophila*, 137
Transcription of the ribosomal RNA gene cluster in *Halobacterium cutirubrum*; multiple promoters, 457
Transcriptional regulation of a periodically controlled flagellar gene operon in *Caulobacter crescentus*, 107
Transcriptional signals from *Escherichia coli*, efficient use in *Bacillus subtilis*, 547
Translational initiation and reinitiation, functional analysis of *lac* repressor restart sites, 733
Translational reinitiation site selection in *lac* repressor mRNA, and mRNA conformation, 725
Transposon-like repeated DNA sequences interspersed in the vitellogenin locus of *Xenopus laevis*; the Vi element, 491
Trapezoid beam profile, analytical estimation of smearing, 172
Travers, A. A. (see also Drew, H. R.), 773
Triturus vulgaris meridionalis (Amphibia, Urodela), molecular organization of ribosomal RNA genes clustered at variable chromosomal sites, 219
Tsugita, A. (see also Keller, B.), 665
Tsukihara, T., Fukuyama, K., Wakabayashi, S., Wada, K., Matsubara, H., Kerscher, L. & Oesterhelt, D., Preliminary X-ray diffraction studies on a ferredoxin from the thermophilic Archaebacterium, *Thermoplasma acidophilum*, 481
Tsuzuki, T. (see also Fukuda, M.), 257
Tuttle, R. W. (see also Chou, K.-C.), 591

Upstream activating sequences in yeast, a region flanking the *GAL7* gene and a binding site for *GAL4* protein, 821
URF1 mitochondrial gene in *Neurospora crassa* has an intron that contains a novel type of URF, 231

Variability in actin genes of *Dictyostelium discoideum*, 321
Vi element. A transposon-like repeated DNA sequence interspersed in the vitellogenin locus of *Xenopus laevis*, 491
Vincent, A., Colot, H. V. & Rosbash, M., Sequence and structure of the *Serendipity* locus of *Drosophila melanogaster*. A densely transcribed region including a blastoderm-specific gene, 149
Virus, influenza, structure and composition; a small-angle neutron scattering study, 565
Viruses, spherical, simulation of scattering from surface spikes, 579
Vitek, M. P. (see also Berger, E. M.), 137
Vitellogenin locus of *Xenopus laevis*, the Vi element: a transposon-like repeated DNA sequence interspersed, 491

Wada, K. (see also Tsukihara, T.), 481
Wahl, W. (see also Schubiger, J.-L.), 491
Wakabayashi, S. (see also Tsukihara, T.), 481
Wakasugi, S. (see also Fukuda, M.), 257
Wallimann, T. (see also Bähler, M.), 381, 393
Wang, J. C. (see also Diekmann, S.), 1
Warwicker, J., Ollis, D., Richards, F. M. & Steitz, T. A., Electrostatic field of the large fragment of *Escherichia coli* DNA polymerase I, 645
Waterman, M. S. (see also Galas, D.), 117
Weber, P. C. (see also Finzel, B. C.), 627
Wei, L.-N. & Joys, T. M., Covalent structure of three phase-1 flagellar filament proteins of *Salmonella*, 791
Werner, S. (see also Burger, G.), 231
Wiley, D. C. (see also Bjorkman, P. J.), 205
Wyckoff, H. W. (see also Sowadski, J. M.), 417

Xenopus laevis, different conformations of ribosomal DNA in active and inactive chromatin, 743
Xenopus laevis: the Vi element, a transposon-like repeated DNA sequence interspersed in the vitellogenin locus, 491
X-ray crystallographic and chromatographic characterization of the crystals of Ca^{2+}-calmodulin complexed with bee venom melittin, 675
X-ray diffraction characterization of bacterial photosynthetic reaction center crystals from *Rhodopseudomonas sphaeroides* R-26, 201
X-ray diffraction studies on the histocompatibility antigens HLA-A2 and HLA-A28 from human cell membranes, 205
X-ray diffraction studies, preliminary, on a ferredoxin from the thermophilic Archaebacterium, *Thermoplasma acidophilum*, 481

Yeast, a region flanking the *GAL7* gene and a binding site for *GAL4* protein as upstream activating sequences, 821

Zauhar, R. J. & Morgan, R. S., A new method for computing the macromolecular electric potential, 815
Zuber, H. (see also Rümbeli, R.), 197